

FIG. 1

LINKER #1 15bp | SV40 ORIGIN=332bp
 GACGTCGGGG CGCGCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
 AGGCCGAGGC GGCGCTGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
 GGAGAATGGG CGGAACCTGGG CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT 180
 ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCACTACTTC TGCGCTGCTGG GGAGCCTGGG 240
 GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
 GGGGAGCCTG GGGACTTTCC ACACCCCTAAC TGACACACAT TCCACAGAAAT TAATTCCCT |
 347 8 360 1
 LINKER #2=13bp
 AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCAT A GCCCATATAT GGAGTTCCGC 420
 GTTACATAAC TTACGGTAAA TGGCCCCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480
 CMV PROMOTER-ENHANCER=567bp
 ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
 TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGT A TCATATGCCA 600
 AGTACGCCCG CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATT TGCCAGTAC 660
 ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
 ATGGTGATGC GGTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTGA CTCACGGGA 780
 TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTGT TTTGGCACCA AAATCAACGG 840
 GACTTTCCAA AATGTCGTA CAACTCCGCC CCATTGACGC AAATGGGCAG TAGGCGTGT 900
 LINKER #3=76bp
 CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
 Bgl II 727 8 LEADER=60bp
 CATCACAGAT CTCTCACCAT 978 9 GAGGGTCCCC GCTCAGCTCC TGGGCTCCT GCTGCTCTGG 1020
 +1 101 102 107 108
 CTCCCAGGTG CACGATGTGA TGGTACCAAG GTGGAAATCA AACGTACGGT GGCTGCACCA 1080
 1038 9 1062 3 Bsi WI
 TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACCTGC CTCTGTTGTG 1140
 TGCCTGCTGA ATAACCTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAAGGT GGATAACGCC 1200
 HUMAN KAPPA CONSTANT 324bp 107 AMINO ACID & STOP CODON
 CTCCAATCGG GTAATCCCAGGAGACTACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1260
 AGCCTCAGCA GCACCCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1320
 TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTCAA CAGGGGAGAG 1380
 STOP
 LIGHT
 CHAIN Eco RI LINKER #4=85bp
 TGTGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC 1440
 1386 7
 GGCGGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500
 1471 2

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GTTCGCCCTTCCCCGTGCC TTCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCCTTCC 1560
TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620
GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680
GCGGTGGGCT CTATGGAACC AGCTGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740
1702 3 1717 8
ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCA GTACATGACC TTATGGACT 1800
TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCCGTTT 1860
CMV PROMOTER-ENHANCER=334bp
GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTCCA AGTCTCCACC 1920
CCATTGACGT CAATGGGAGT TTGTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980
GTAACAACTC CGCCCCATTG ACGAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
LINKER #6=7bp
TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2100
2051 2 2058 9 LEADER=51bp Mu I 2151 2 Nhe I
ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACGCGTGT CGCTAGGACC 2160
START HEAVY CHAIN -5 -4 -3 114 115
AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACACCG 2220
GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCCG TGACGGTGTG GTGGAACCTCA 2280
GGCGCCCTGA CCAGCGGCGT GCACACCTTC CGGGCTGTCC TACAGTCCTC AGGACTCTAC 2340
HUMAN GAMMA 1 CONSTANT
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 2400
993bp=330 AMINO ACID & STOP CODON
AACGTGAATC ACAAGCCCCAG CAACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT 2460
GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 2520
TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACCA 2580
TGCCTGGTGG TGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640
GGCGTGGAGG TGCATAATGC CAAGACAAAG CGCGGGAGG AGCAGTACAA CAGCACGTAC 2700
CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGACTACAAG 2760
TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820
GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCAT CCCGGGATGA GCTGACCAGG 2880
AACCAAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 2940
TGGGAGAGCA ATGGGCAGCC GGAGAACACCA TACAAGACCA CGCCTCCCGT GCTGGACTCC 3000

FIG. 2B

GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 3060
 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120
 STOP HEAVY CHAIN Bam HI LINKER #7=81bp
 CTCTCCCTGT CTCCGGGTAA ATGAGGATCC GTTAACGGTT ACCAACTACC TAGACTGGAT 3180
 3144 5
 TCGTGACAAC ATGCGGCCGT GATATCTACG TATGATCAGC CTCGACTGTG CCTTCTAGTT 3240
 3225 6
 GCCAGCCATC TGTTGTTGC CCCTCCCCCG TGCTTCCTT GACCTGGAA GGTGCCACTC 3300
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 CCACTGTCTT TTCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT 3360
 CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGAA GACAATACCA 3420
 GGCATGCTGG GGATGCGGTG GGCTCTATGG AACCAGCTGG GGCTCGACAG CGCTGGATCT 3480
 3456 7
 CCCGATCCCC AGCTTGCTT CTCATAATTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 3540
 3490 1
 AATTTAACCA CCAATTCACT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 3600
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 3660
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 3720
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAAGAGAGG 3780
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 3840
 CTGACATAGT TGTGTTGGGA GCTTGGATAG CTTGGACAGC TCAGGGCTGC GATTTGGCGC 3900
 3856 7 3875 6
 START DHFR
 CAAACTTGAC GGCAATCCTA GCGTGAAGGC TGTTAGGATT TTATCCCCGC TGCCATCATT 3960
 3957 8
 GTTCGACCAT TGAACCTGCAT CGTCGCCGTG TCCCCAAATA TGGGGATTGG CAAGAACCGA 4020
 GACCTACCCCT GGCTCCGCT CAGGAACGAG TTCAAGTACT TCCAAAGAAT GACCACAAACC 4080
 TCTTCAGTGG AAGGTAAACA GAATCTGGTG ATTATGGGTAA GGAAAACCTG GTTCTCCATT 4140
 MOUSE DHFR=564bp=187 AMINO ACID & STOP CODON
 CCTGAGAAGA ATCGACCTTT AAAGGACAGA ATTAATATAG TTCTCAGTAG AGAACTCAAA 4200
 GAACCACCAAC GAGGAGCTCA TTTTCTTGCC AAAAGTTGG ATGATGCCTT AAGACTTATT 4260
 GAACAACCGG AATTGGCAAG TAAAGTAGAC ATGGTTGGA TAGTCGGAGG CAGTTCTGTT 4320
 TACCAAGGAAG CCATGAATCA ACCAGGCCAC CTTAGACTCT TTGTGACAAG GATCATGCAG 4380
 GAATTTGAAA GTGACACGTT TTTCCCAGAA ATTGATTGG GGAAATATAA ACTTCTCCCA 4440
 GAATACCCAG GCGTCCTCTC TGAGGTCCAG GAGGAAAAAG GCATCAAGTA TAAGTTGAA 4500

FIG. 2C

STOP DHFR
 GTCTACGAGA AGAAAGAC~~T~~A ACAGGAAGAT GCTTTCAAGT TCTCTGCTCC CCTCCTAAAG 4560
 4521 2

3' UNTRANSLATED DHFR=82bp
 TCATGCATT TTATAAGACC ATGGGACTTT TGCTGGCTTT AGATCAGCCT CGACTGTGCC 4620
 4603 4 4613 4

LINKER #10=10bp
 TTCTAGTTGC CAGCCATCTG TTGTTGCC CTCCTCGTG CCTTCCTTGA CCCTGGAAAGG 4680

BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 TGCCACTCCC ACTGTCCTT CCTAATAAAA TGAGGAATT GCATCGCATT GTCTGAGTAG 4740

GTGTCATTCT ATTCTGGGGG GTGGGGTGGG GCAGGACAGC AAGGGGGAGG ATTGGGAAGA 4800

LINKER #11=17bp
 CAATAGCAGG CATGCTGGGG ATGCGGTGGG CTCTATGGAA CCAGCTGGGG CTCGAGCTAC 4860
 4844 5

TAGCTTGCT TCTCAATTTC TTATTTGCAT AATGAGAAAA AAAGGAAAAT TAATTTAAC 4920

ACCAATTCAAG TAGTTGATTG AGCAAATGCG TTGCCAAAAAA GGATGCTTTA GAGACAGTGT 4980

MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 TCTCTGCACA GATAAGGACA AACATTATTC AGAGGGAGTA CCCAGAGCTG AGACTCCTAA 5040

GCCAGTGAGT GGCACAGCAT TCTAGGGAGA AATATGTTG TCATCACCGA AGCCTGATTG 5100

CGTAGAGCCA CACCTTGGTA AGGGCCAATC TGCTCACACA GGATAGAGAG GGCAGGAGCC 5160

AGGGCAGAGC ATATAAGGTG AGGTAGGATC AGTTGCTCCT CACATTGCT TCTGACATAG 5220

LINKER #12=21bp
 TTGTGTTGGG AGCTTGGATC GATCCTCTAT~~T~~GGTTGAACAA GATGGATTGC ACGCAGGTTTC 5280
 5227 8 5248 9

START NEO

TCCGGCCGCT TGGGTGGAGA GGCTATTGG CTATGACTGG GCACAAACAGA CAATCGGCTG 5340

CTCTGATGCC GCCGTGTTCC GGCTGTCAGC GCAGGGGCGC CCGGTTCTTT TTGTCAAGAC 5400

NEOMYCIN PHOSPHOTRANSFERASE
 CGACCTGTCC GGTGCCCTGA ATGAACGTGCA GGACGAGGCA GCGGGGCTAT CGTGGCTGGC 5460

795bp=264 AMINO ACIDS & STOP CODON
 CACGACGGGC GTTCCTTGCG CAGCTGTGCT CGACGTTGTC ACTGAAGCGG GAAGGGACTG 5520

GCTGCTATTG GGCGAAGTGC CGGGGCAGGA TCTCCTGTCA TCTCACCTTG CTCCGTCCG 5580

GAAAGTATCC ATCATGGCTG ATGCAATGCG GCGGCTGCAT ACGCTTGATC CGGCTACCTG 5640

CCCATTGAC CACCAAGCGA AACATCGCAT CGAGCGAGCA CGTACTCGGA TGGAAAGCCGG 5700

TCTTGTGAT CAGGATGATC TGGACGAAGA GCATCAGGGG CTCGCGCCAG CCGAACTGTT 5760

CGCCAGGCTC AAGGCGCGCA TGCCCCACGG CGAGGATCTC GTCGTGACCC ATGGCGATGC 5820

CTGCTTGCCG AATATCATGG TGGAAAATGG CCGCTTTCT GGATTGATCG ACTGTGGCCG 5880

GCTGGGTGTG GCGGACCGCT ATCAGGACAT AGCGTTGGCT ACCCGTGATA TTGCTGAAGA 5940

GCTTGGCGGC GAATGGGCTG ACCGCTTCCT CGTGCTTTAC GGTATCGCCG CT~~T~~CCCGATTG 6000

FIG. 2D

GCAGCGCATC GCCTTCTATC GCCTTCTTGA CGAGTTCTTC **STOP NEO¹**
 6043 4 TGAGGGGAC TCTGGGGTTC 6060
 GAAATGACCG ACCAAGCGAC GCCCAACCTG CCATCACGAG ATTCGATT CACCGCCGCC 6120
 3' UNTRANSLATED NEO=173bp
 TTCTATGAAA GGTTGGGCTT CGGAATCGTT TTCCGGGACG CCGGCTGGAT GATCCTCCAG 6180
 CGCGGGGATC TCATGCTGGA GTTCTTCGCC CACCCCCAACT TGTTTATTGC AGCTTATAAT 6240
 6216 7
 GGTTACAAAT AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTC TTCACTGCAT 6300
 SV40 POLY A EARLY=133bp LINKER #13=19bp
 TCTAGTTGTG GTTTGTCCAA ACTCATCAAT CTATCTTATC ATGTC~~TGGAT~~ CGCGGCCGCG 6360
 6349 50
 ATCCCGTGGA GAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC 6420
 6368 9
 CGCTCACAAAT TCCACACAAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT 6480
 AATGAGTGAG CTAACTCACA TTAATTGCGT TGCGCTCACT GCCCGCTTTC CAGTCGGGAA 6540
 ACCTGTCTG CCAGCTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCCTA 6600
 PVC 19
 TTGGGGCGCTC TTCCGCTTCC TCGCTCACTG ACTCGCTGCG CTCGGTCGTT CGGCTGCCTG 6660
 GAGCGGTATC AGCTCACTCA AAGGCGGTAA TACGGTTATC CACAGAATCA GGGGATAACG 6720
 CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG GAACCGTAHA AAGGCCGCGT 6780
 6792=BACTERIAL ORIGIN OF REPLICATION
 TGCTGGCGTT T~~T~~TCCATAGG CTCCGCCCCC CTGACGAGCA TCACAAAAAT CGACGCTCAA 6840
 GTCAGAGGTG GCGAAACCCG ACAGGACTAT AAAGATACCA GGCCTTCCC CCTGGAAGCT 6900
 CCCTCGTGCG CTCTCCTGTT CCGACCCCTGC CGCTTACCGG ATACCTGTCC GCCTTCTCC 6960
 CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG 7020
 TCGTTCGCTC CAAGCTGGC TGTGTGCACG AACCCCCCGT TCAGCCGAC CGCTGCCTG 7080
 TATCCGGTAA CTATCGTCTT GAGTCCAACC CGGTAAAGACA CGACTTATCG CCACTGGCAG 7140
 CAGCCACTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA 7200
 AGTGGTGGCC TAACTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA 7260
 AGCCAGTTAC CTTCGGAAAA AGAGTTGGTA GCTCTTGATC CGGCAAACAA ACCACCGCTG 7320
 GTAGCGGTGG TTTTTTGTT TGCAAGCAGC AGATTACGGC CAGAAAAAAA GGATCTCAAS 7380
 AAGATCCTTT GATCTTTCT ACGGGGTCTG ACGCTCAGTG GAACGAAAAC TCACGTTAAG 7440
 GGATTTGGT CATGAGATTA TCAAAAAGGA TCTTCACCTA GATCCTTTA AATTAAAAAT 7500

FIG. 2E

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STOP BETA LACTAMASE
GAAGTTTAA ATCAATCTAA AGTATATATG AGTAAACCTTG GTCTGACAGT TACCAATGCT 7560
7550
TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTCG TTCATCCATA GTTGCTGAC 7620
TCCCCGTGCGT GTAGATAACT ACGATAACGGG AGGGCTTACC ATCTGGCCCC AGTGCTGCAA 7680
TGATACCGCG AGACCCACGC TCACCGGCTC CAGATTATC AGCAATAAAC CAGCCAGCCG 7740
GAAGGGCCGA GCGCAGAAGT GGTCCTGCAA CTTTATCCGC CTCCATCCAG TCTATTAATT 7800
BETA LACTAMASE=861bp
286 AMINO ACID & STOP CODON
GTTGCCGGGA AGCTAGAGTA AGTAGTTCGC CAGTTAATAG TTTGCGCAAC GTTGTGCCA 7860
TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTGGTAT GGCTTCATTC AGCTCCGGTT 7920
CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAAGCG GTTAGCTCCT 7980
TCGGTCCTCC GATCGTTGTC AGAAGTAAGT TGGCCGAGT GTTATCACTC ATGGTTATGG 8040
CAGCACTGCA TAATTCTCTT ACTGTCATGC CATCCGTAAG ATGCTTTCT GTGACTGGTG 8100
AGTACTCAAC CAAGTCATTC TGAGAATAGT GTATGCGGCG ACCGAGTTGC TCTTGCCCGG 8160
CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA 8220
AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTCGATGT 8280
AACCCACTCG TGCACCCAAC TGATCTTCAG CATCTTTAC TTTCACCAAGC GTTCTGGGT 8340
GAGCAAAAAC AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT 8400
START BETA LACTAMASE
GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
8410
TGAGCGGATA CATATTTGAA TGTATTTAGA AAAATAAACAA AATAGGGGTT CCGCGCACAT 8520
TTCCCCGAAA AGTGCCACCT

FIG. 2F

LINKER #1=15bp
 GACGTCGGGG CGCGCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTAG 50
 15' 6

AGGCCGAGGC GGCGCTGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGCGATGGGGC 120
 SV40 ORIGIN=332bp
 GGAGAATGGG CGGAACCTGGG CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT 180
 ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCGATACTTC TGCGCTGCTGG GGAGCCTGGG 240
 GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
 GGGGAGCCTG GGGACTTTCC ACACCCCTAAC TGACACACAT TCCACAGAAAT TAATTCCCCT 360
 347' 8
 LINKER #2=13bp

AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCAT A GCCCATATAT GGAGTTCCGC 420
 GTTACATAAC TTACGGTAAA TGGCCCCCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480
 ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTCCA TTGACGTCAA 540
 CVM PROMOTER-ENHANCER=567bp
 TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGT A TCATATGCCA 600
 AGTACGCCCT CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATT TGCCCAGTAC 660
 ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
 ATGGTGATGC GGTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTGA CTCACGGGG 780
 TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTGT TTTGGCACCA AAATCAACGG 840
 GACTTTCCAA AATGTCGTA CAACCTCCGCC CCATTGACGC AAATGGCGG TAGGCGTGT 900
 CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
 927' 8 934' 5

Bgl 2 START LIGHT CHAIN NATURAL LEADER=66bp
 CATCACAGAT CTCTCACTAT G GATTTTCAG GTGCAGATT TGAGCTTCCT GCTAACTAGT 1020
 978' 9

GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT 1080
 1044' 5 +1

GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAAGGCCA GCTGAAGTGT AAGTTACATC 1140
 CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCCCT GGATTTATGC CACATCCAAC 1200
 LIGHT CHAIN VARIABLE REGION 318bp 106 AMINO ACID
 CTGGCTTCTG GAGTCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTACTCTCTC 1260
 ACCATCAGCA GAGTCGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT 1320
 AACCCACCCA CGTTGGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCACCA 1380
 1362' 3

BsiWI
 TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACTGC CTCTGTTGTG 1440
 TGCGCTGCTGA ATAACCTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAAGGT GGATAACGCC 1500

FIG. 3A

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HUMAN KAPPA CONSTANT=324bp=107 AMINO ACID & STOP CODON
CTCCAATCGG GTAACTCCCA GGAGAGTGT ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1560
AGCCTCAGCA GCACCCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1620
TGCAGAAGTCACCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1680
STOP
LIGHT
CHAIN Eco RI LINKER #4=81bp
TGT~~TGA~~ATTCA AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC 1740
1646 7
GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1800
1771 2
GTTTGCCCCCT CCCCCGTGCC TTCCCTGACC CTGGAAGGTG CCACCTCCAC TGTCCTTCC 1860
TAATAAAATG AGGAAATTGC ATCGCATTTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1920
BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1980
LINKER #5=15bp
GCGGTGGGCT CTATGGAACC AGCTGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 2040
2002 3 2017 8
ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 2100
TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 2160
CMV PROMOTER-ENHANCER=334bp
GGCAGTACAT CAATGGCGT GGATAGCGGT TTGACTCACCG GGGATTCCA AGTCTCCACC 2220
CCATTGACGT CAATGGGAGT TTGTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 2280
GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGGCG TGTACCGTGG GAGGTCTATA 2340
LINKER #6=7bp Sal I
TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2400
START 2351 2 2358 9
HEAVY CHAIN SYNTHETIC & NATURAL LEADER Mlu I 2457 8
ATGGGTTGGCA GCCTCATCTT GCTCTTCTT GTCGCTGTT CTACCGTGT CCTGTCCAG 2460
2401 -5 -4 -3 -2 -1 +1
GTACAACTGC AGCAGCCTGG GGCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATGTCC 2520
TGCAAGGCTT CTGGCTACAC ATTTACCACT TACAATATGC ACTGGGTAAA ACAGACACCT 2580
HEAVY CHAIN VARIABLE=363bp=121 AMINO ACID
GGTCGGGGCC TGGAATGGAT TGGAGCTATT TATCCCGGAA ATGGTGATAC TTCCTACAAT 2640
CAGAAGTTCA AAGGCAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 2700
CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ACTGTGCAAG ATCGACTTAC 2760
TACGGCGGTG ACTGGTACTT CAATGTCTGG GGCAGCAGGGCA CCACGGTCAC CGTCTCTGCA 2820
Nhe I
GCTAGCACCA AGGGCCCACATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG 2880
GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTG 2940
HUMAN GAMMA 1 CONSTANT=993bp
TGGAACTCAG GCGCCCTGAC CAGCGGGCGTG CACACCTTCC CGGCTGTCT ACAGTCCTCA 3000

FIG. 3B

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330 AMINO ACID & STOP CODON
GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 3060
TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGCAGAGCCC 3120
AAATCTTGTG ACAAAACTCA CACATGCCA CCGTGCCCCAG CACCTGAACt CCTGGGGGGA 3180
CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT 3240
GAGGTACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG 3300
TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC 3360
AGCACGTACC GTGTGGTCAG CGTCCTCACCC GTCTGCACC AGGACTGGCT GAATGGCAAG 3420
GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCS CCATCGAGAA AACCATCTCC 3480
AAAGCCAAAG GGCAGCCCCG AGAACACACAG GTGTACACCC TGCCCCCATC CCGGGATGAG 3540
CTGACCAAGA ACCAGGTCAAG CCTGACCTGC CTGGTCAAAG GCTTCTATCC CAGCGACATC 3600
GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAACT ACAAGACCAC GCCTCCCGTG 3660
CTGGACTCCG ACGGCTCCTT CTTCTCTAC AGCAAGCTCA CCGTGGACAA GAGCAGGTGG 3720
CAGCAGGGGA ACGTCTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG 3780
CAGAAGAGCC TCTCCCTGTC TCCGGTAAA [TGAGGATCCG TTAACGGTTA CCAACTACCT 3840
3813 4 STOP HEAVY CHAIN |Bam HI LINKER #7=81bp
AGACTGGATT CGTGACAACA TGCAGCCCGTG ATATCTACGT ATGATCAGCC TCGACTGTGC 3900
3894 5 CTTCTAGTTG CCAGCCATCT GTTGTGTTGCC CCTCCCCGT GCCTTCCTTG ACCCTGGAA 3960
GTGCCACTCC CACTGTCCTT TCCTAATAAA ATGAGGAAAT TGCAATCGCAT TGTCTGAGTA 4020
BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
GGTGTCAATT TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGGAAG 4080
ACAATAGCAG GCATGCTGGG GATGCGGTGG GCTCTATGGA ACCAGCTGGG GCTCGACAGC 4140
4125 6 GCTGGATCTC CCGATCCCCA GCTTGCTTC TCAATTCTT ATTTGCATAA TGAGAAAAAA 4200
AGGAAAATTA ATTTAACAC CAATTCAAGTA GTTGATTGAG CAAATGCGTT GCCAAAAAAGG 4260
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
ATGCTTTAGA GACAGTGGTC TCTGCACAGA TAAGGACAAA CATTATTCAAG AGGGAGTACC 4320
CAGAGCTGAG ACTCCTAACGC CAGTGAGTGG CACAGCATTG TAGGGAGAAA TATGCTTGTG 4380
ATCACCGAAG CCTGATTCCG TAGAGCCACA CCTGGTAAG GGCAATCTG CTCACACAGG 4440
ATAGAGAGGG CAGGAGCCAG GGCAGAGCAT ATAAGGTGAG GTAGGATCAG TTGCTCCTCA 4500

FIG. 3C

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CATTTGCTTC TGACATAGTT LINKER #9=19bp 5' UNTRANSLATED DHFR=82bp
4525 6 4544 5
ATTTCGCGCC AAACTTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATT TATCCCCGCT 4520
START DHFR
GCCATC~~TATGG~~ TTGGACCATT GAACTGCATC GTCGCCGTGT CCCAAAATAT GGGGATTGGC 4680
4626 7
AAGAACGGAG ACCTACCCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740
ACCACAAACCT CTTCACTGGA AGGTAAACAG AATCTGGTGA TTATGGTAG GAAAACCTGG 4800
DHFR=564bp=187 AMINO ACID & STOP CODON
TTCTCCATTG CTGAGAAGAA TCGACCTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860
GAACTCAAAG AACCAACCACG AGGAGCTCAT TTTCTTGCCA AAAGTTTGGG TGATGCCCTA 4920
AGACTTATTG ACAACCGGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980
AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040
ATCATGCAGG AATTGAAAG TGACACGTTT TTCCCAGAAA TTGATTTGGG GAAATATAAA 5100
CTTCTCCAG AATACCCAGG CGTCCTCTCT GAGGTCCAGG AGGAAAAAGG CATCAAGTAT 5160
STOP DHFR 3' UNTRANSLATED DHFR=82bp
AAGTTTGAAG TCTACGAGAA GAAAGACTAA CAGGAAGATG CTTCAAGTT CTCTGCTCCC 5220
5140 1
CTCCTAAAGC TATGCATTT TATAAGACCA TGGGACTTT GCTGGCTTA GATCAGCCTC 5280
=10bp] 5272 3
GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTGCCCC TCCCCCGTGC CTTCTTGAC 5340
BOVINE GROWTH HORMONE POLYADENYLATION=231bp
CCTGGAAAGGT GCCACTCCC CTGTCCTTTC CTAATAAAAT GAGGAAATTG CATCGCATIG 5400
TCTGAGTAGG TGTCAATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460
TTGGGAAGAC AATAGCAGGC ATGCTGGGA TGCAGGTGGC TCTATGGAAC CAGCTGGGGC 5520
5513 4
=17bp TCGAGCTACT AGCTTTGCTT CTCATTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 5580
5530 1
AATTTAACCA CCAATTCACT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 5640
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
AGACAGTGTG CTCTGCACAG ATAAGGACAA CTAGGGAGAA ATATGCTTGT CATCACCGAA 5700
GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 5760
GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820
GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCCTCTC ACATTTGCTT 5880
LINKER #12=21bp START NEO
CTGACATAGT TGTGTTGGGA GCTTGGATCG ATCCTCTATG GTTGAACAAG ATGGATTGCA 5940
5896 7 5917 8
CGCAGGTTCT CGGGCCGCTT GGGTGGAGAG GCTATTGGC TATGACTGGG CACAAACAGAC 6000

FIG. 3D

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AATCGGCTGC TCTGATGCCG CCGTGTCCG GCTGTCAGCG CAGGGGCG:G CGGTTCTTT 6060
NEOMYCIN PHOSPHOTRANSFERASE=795bP=264 AMINO ACID & STOP CODON
TGTCAAGACC GACCTGTCCG GTGCCCTGAA TGAACGTGAG GACGAGGCAG CGCGGCTATC 6120
GTGGCTGGCC ACGACGGGCG TTCCCTTGCGC AGCTGTGTC GACGTTGTCA CTGAAGCGGG 6180
AAGGGACTGG CTGCTATTGG GCGAAGTGCC GGGGCAGGAT CTCCTGTCA CAT CTCACCTTGC 6240
TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCCG CGGCTGCATA CGCTTGATCC 6300
GGCTACCTGC CCATTGACCC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360
GGAAGCCGGT CTTGTCGATC AGGATGATCT GGACGAAGAG CATCAGGGC TCGCGCCAGC 6420
CGAACTGTTG GCCAGGCTCA AGGCGCGCAT GCCCGACGGC GAGGATCTCG TCGTGACCCA 6480
TGGCGATGCC TGCTTGCGA ATATCATGGT GGAAAATGGC CGCTTTCTG GATTGATCGA 6540
CTGTGGCCGG CTGGGTGTGG CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT 6600
TGCTGAAGAG CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTAAAG GTATCGCC 6660
STOP NEO
TCCCGATTG CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTTC~~T~~ GAGCGGGACT 6720
6712 3
CTGGGGTTCG AAATGACCGA CCAAGCGACG CCCAACCTGC CATCACGAGA TTTGATTCC 6780
3' UNTRANSLATED NEO=173bp
ACCGCCGCCT TCTATGAAAG GTTGGGCTTC GGAATCGTT TCCGGGACCC CGGCTGGATG 6840
ATCCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTCGCCCC ACCCCAAACTT GTTTATTGCA 6900
6885 6
GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATA> AGCATTTC 6960
SV40 EARLY POLYADENYLATION REGION=133bp
TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATC TATCTTATCA TGTCTGGATC 7020
7018 9
LINKER #13=19bp
GCGGCCGCGA TCCCGTGCAG AGCTTGGCGT AATCATGGTC ATAGCTGTT CCTGTGTGAA 7080
7037 8 PUC 19
ATTGTTATCC GCTCACAAATT CCACACAAACA TACGAGCCGG AAGCATAAAG TGTAAAGCCT 7140
GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTCC 7200
AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACCGCGG GGGAGAGGCG 7260
GTTTGCCTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCC TCGGTGTTTC 7320
GGCTGCCGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTA~~TCC~~ ACAGAATCAG 7380
GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAUG AACCGTAAAA 7440
7461=BACTERIAL ORIGIN OF REPLICATION
AGGCCCGCTT GCTGGCGTT TCCATAGGC TCCGCCCCCCC TGACGAGCAT CACAAAAATC 7500

FIG. 3E

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GACGCTCAAG TCAGAGGTGG CGAAACCGA CAGGACTATA AAGATACCAG GCGTTCCCC 7560
CTGGAGCTC CCTCGTGCAC TCTCCTGTTC CGACCCCTGCC GCTTACCGGA TACCTGTCCG 7620
CCTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT 7680
CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGAC 7740
GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC 7800
CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860
AGTTCTTGAA GTGGTGGCCT AACTACGGCT ACACATAGAAG GACAGTATTG GGTATCTGCG 7920
CTCTGCTGAA GCCAGTTACC TTGGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA 7980
CCACCGCTGG TAGCGGTGGT TTTTTGTTT GCAAGCAGCA GATTACGCCG AGAAAAAAAG 8040
GATCTCAAGA AGATCCTTG ATCTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAAC 8100
CACGTTAAGG GATTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTAA 8160
STOP
ATTAAGGAAAGTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGT 8220
BETA LACTAMASE
ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTCGT TCATCCATAG 8280
TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATAACGGGA GGGCTTACCA TCTGGCCCCA 8340
GTGCTGCAAT GATAACCGCA GACCCACGCT CACCGGCTCC AGATTATCA GCAATAAAC 8400
BETA LACTAMASE=861bp=286 AMINO ACID & STOP CODON
AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCTGCAAC TTTATCCGCC TCCATCCAGT 8460
CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTGCC AGTTAATAGT TTGCGCAACG 8520
TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTGGTATG GCTTCATTCA 8580
GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8640
TTAGCTCCTT CGGTCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA 8700
TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTCTG 8760
TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCCGGCA CCGAGTTGCT 8820
CTTGCCCCGGC GTCAATAACGG GATAATAACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA 8880
TCATTGGAAA ACGTTCTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940
GGTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTACT TTCACCAGCG 9000
TTTCTGGGTG AGCAAAAACA GGAAGGCCAAA ATGCCGAAA AAAGGGAATA AGGGCGACAC 9060
GGAAATGTTG AATACTCATC CTCTTCCTTT TTCAATATTAA TTGAAGCATT TATCAGGGTT 9120
ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC 9180
CGCGCACATT TCCCCGAAAA GTGCCACCT

FIG. 3F

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LEADER

	-20		-15		-10		
FRAME 1	Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val						
	ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC						
	987	996	1005	1014	1023		
	5	6					
	FR1						
	Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser						
	ATA ATG TCC AGA GGA CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT						
	1038	1047	1056	1065	1074	1083	
	20	23	24	CDR1	27	29	30
Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His							
CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA AGT TAC ATC CAC							
1095	1104	1113	1122	1131	1140		
35 FR2	40	45	49	50	CDR2		
Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn							
TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT GCC ACA TCC AAC							
1152	1161	1170	1179	1188	1197		
55 56	57	60	FR3	65	70		
Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser							
CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC AGT GGG TCT GGG ACT TCT TAC TCT							
1209	1218	1227	1236	1245	1254		
75	80	85					
Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp							
CTC ACC ATC AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG							
1266	1275	1284	1293	1302	1311		
CDR3 95	97	98	100 FR4	105	107		
Thr Ser Asn Pro Pro Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys							
ACT AGT AAC CCA CCC ACG TTC GGA GGG ACC AAC CTG GAA ATC AAA							
1323	1332	1341	1350	1359			

FIG. 4

LEADER

-19	-15	-10	-5		
FRAME 1 Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val					
ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC					
2409	2418	2427	2436		
2445					
-1 +1	FR1	10	15		
Leu Ser	Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys	Ala	Gly Ala Ser		
CTG TCC	CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG GCC TCA				
2460	2469	2478	2487		
			2496 GCT		
			2505		
20	25	30	31 CDR1	35	36
Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr		Ser Tyr Asn Met His	Trp		
GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC		AGT TAC AAT ATG CAC	TGG		
2517	2526	2536	2541	2553	2562
40 FR2	45	49	50	52 52A	53 54
Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly		Ala Ile Tyr Pro Gly Asn			
GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA		GCT ATT TAT CCC GGA AAT			
2574	2583	2592	2601	2610	2619
55 CDR2	60	65	66 FR3	70	
Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly	Lys Ala Thr Leu Thr Ala Asp Lys				
GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC	AAG GCC ACA TTG ACT GCA GAC AAA				
2631	2640	2649	2658	2667	2676
75	80	82 82A 82B 82C 83	85		
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val					
TCC TCC AGC ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC					
2688	2697	2706	2715	2724	2733
90	94 95	CDR3	100 100A 100B 100C 100D 101	102 103	
Tyr Tyr Cys Ala Arg	Ser Thr Tyr Tyr Gly Gly Asn Trp Tyr Phe Asn Val	Trp	Gly		
TAT TAC TGT GCA AGA	TCG ACT TAC TAC GGC GGT GAC TGG TAC TTC AAT GTC	TGG	GTC	TGG GGC	
2745	2754	2763	2772	2781	2790
105 FR4	110	113			
Ala Gly Thr Thr Val Thr Val Ser Ala					
GCA GGG ACC ACG GTC ACC GTC TCT GCA					
2802	2811	2820			

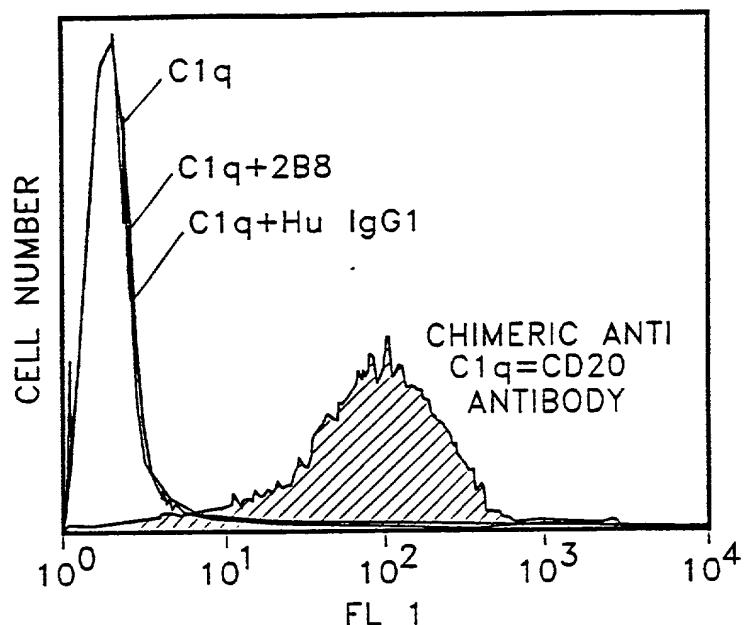


FIG. 6

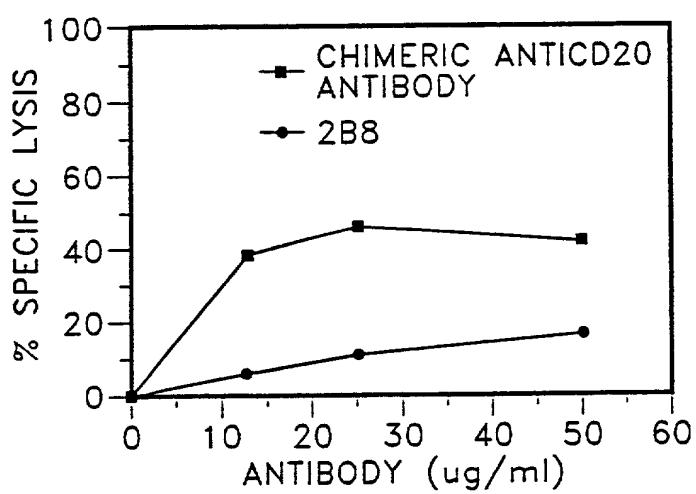


FIG. 7

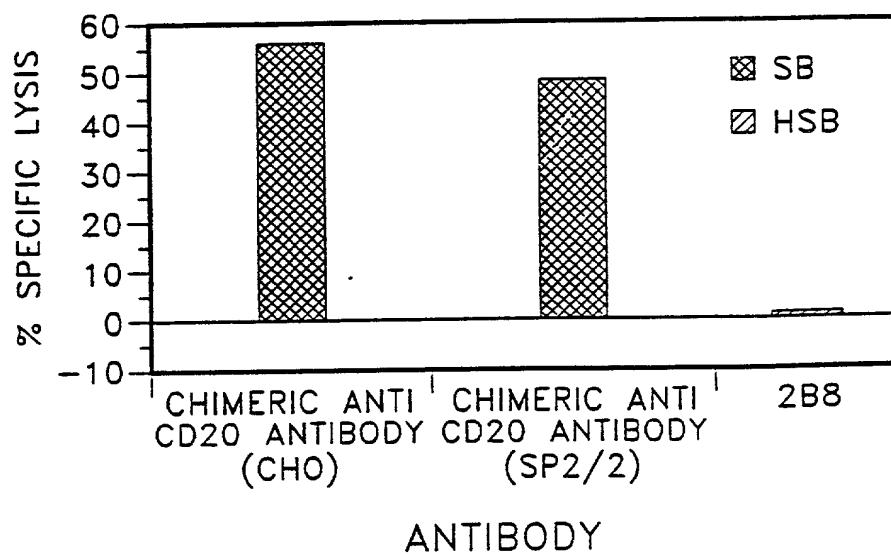


FIG. 8

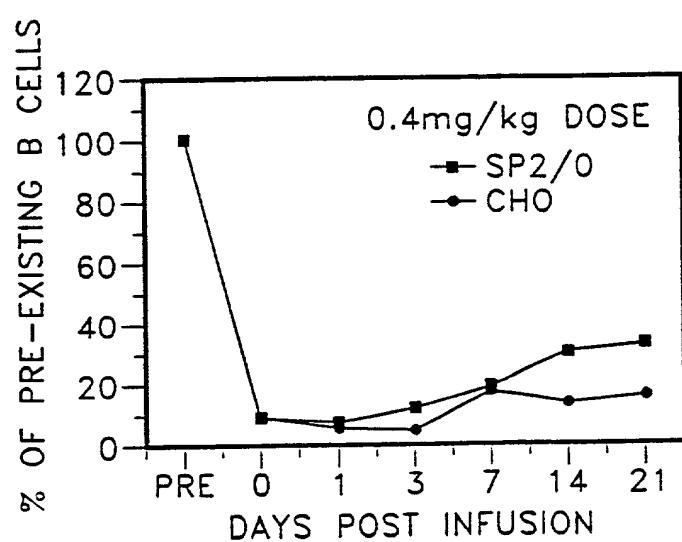


FIG. 9A

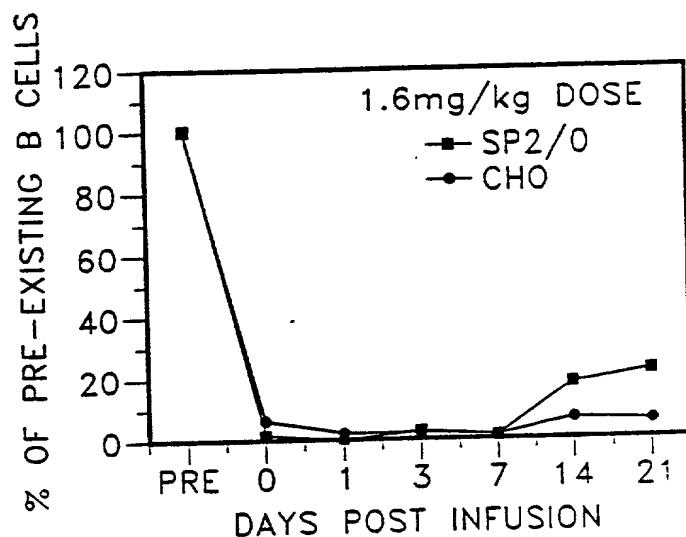


FIG. 9B

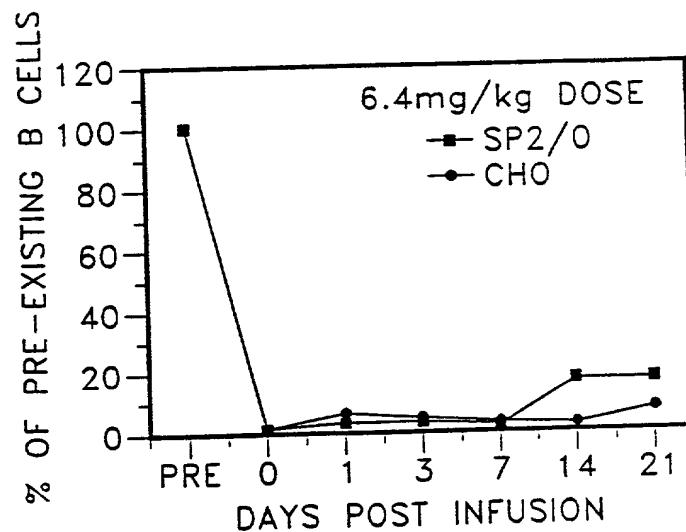


FIG. 9C

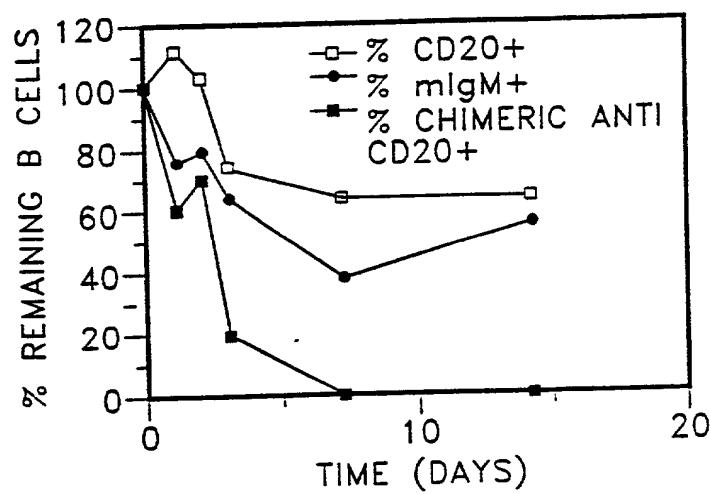


FIG. 10

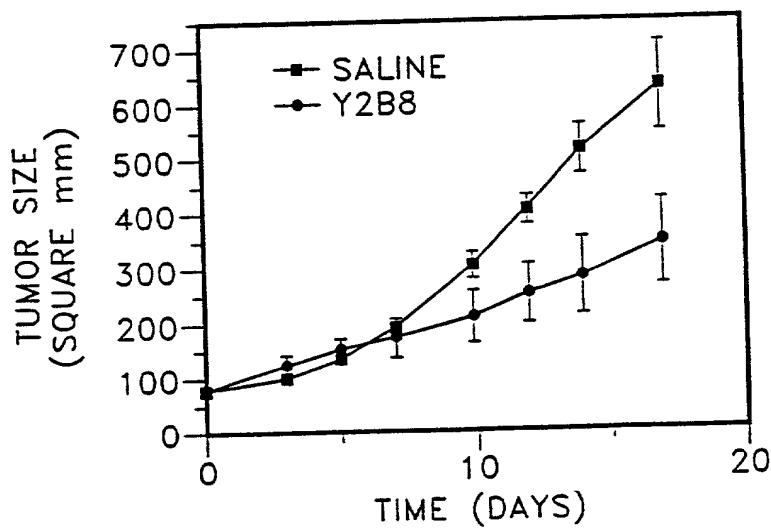


FIG. 11

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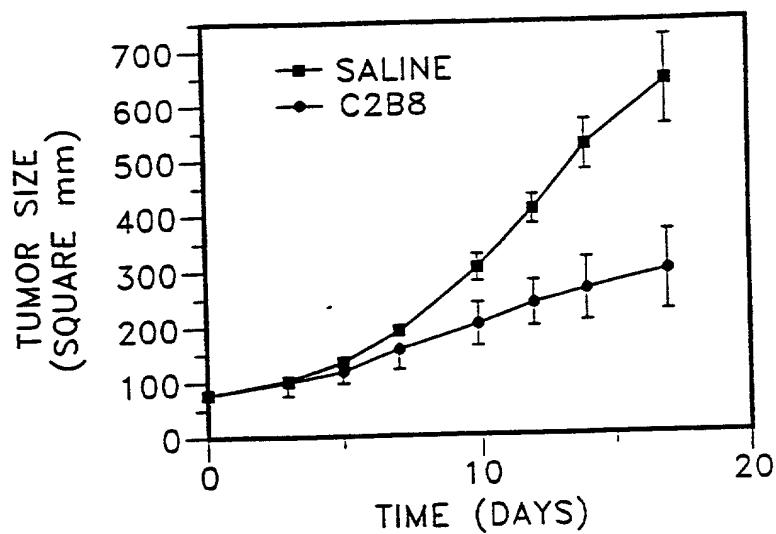


FIG. 12

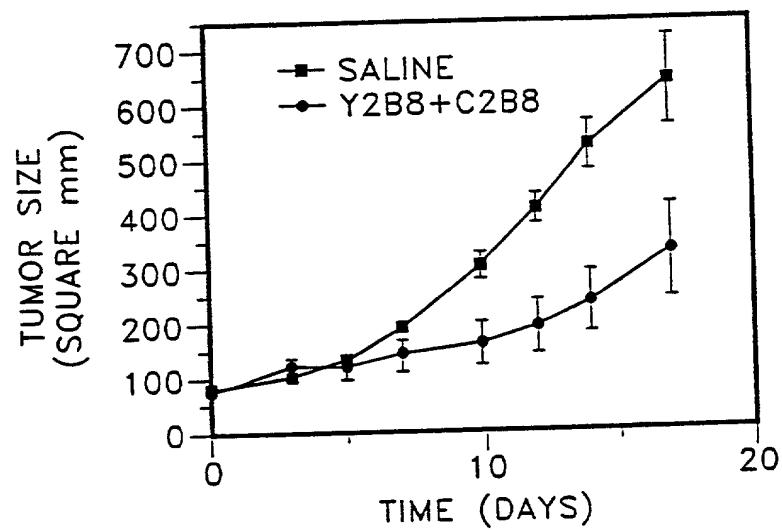


FIG. 13

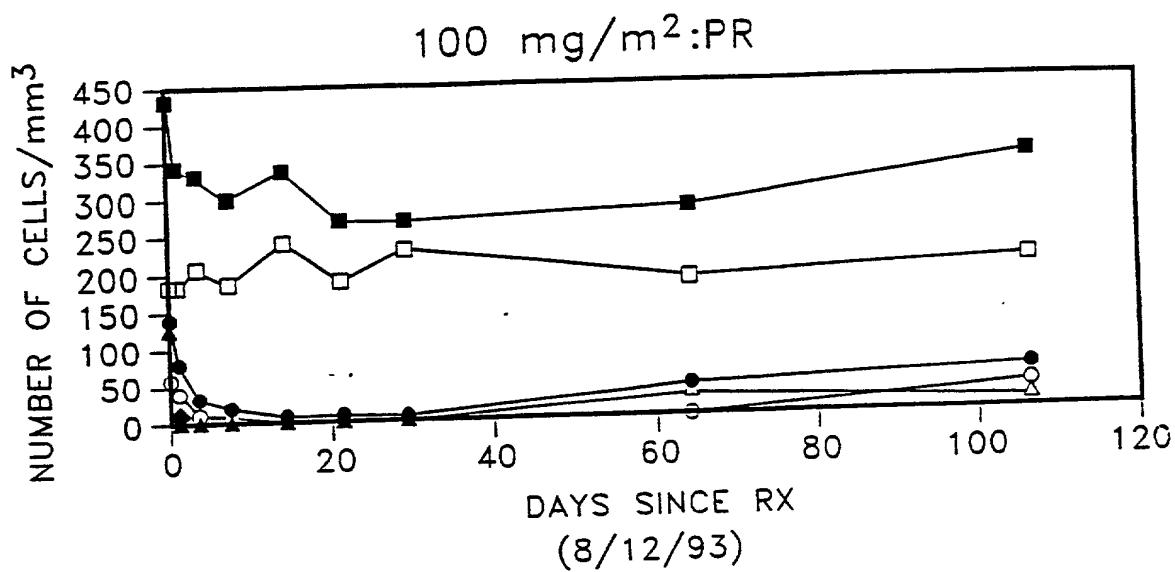


FIG. 14A

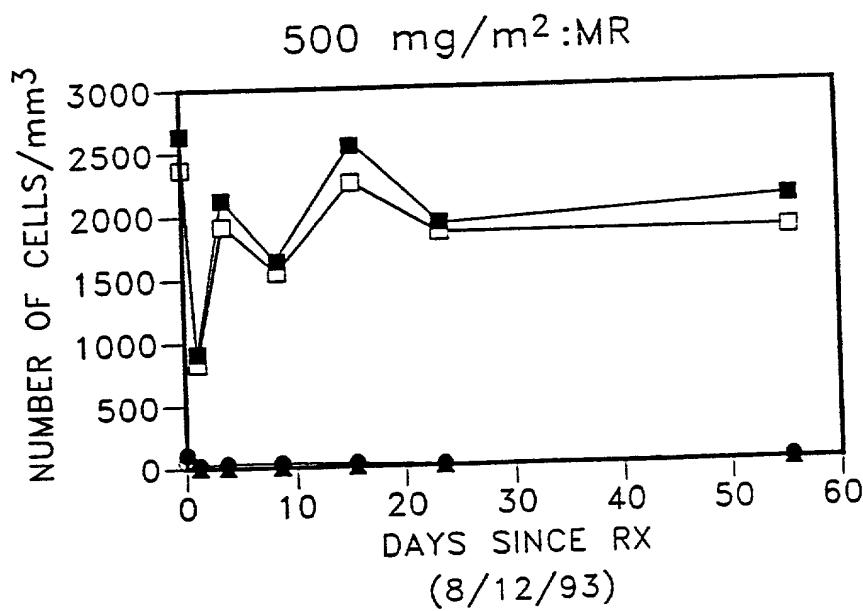


FIG. 14B